

**Amendments to the Specification:**

**Replace the paragraph 0128 with the following:**

[0128] The EBV genome is a 170-kilobase linear DNA molecule that consists of largely unique DNA domains( U1,U2,U3,U4,and U5), as shown in Fig. 1[.], with internal ~~Internal~~ tandem direct repeats (IR1, IR2, IR3, IR4), and terminal repeats (TR). In latently infected cells, the complete viral genome persists as episomes or integrated DNA. The expression of viral genome is limited. However at least three sites on the viral genome are characteristically transcribed:

- I. IR1 into U2
- II. U3 through IR3 into U4
- III. From U5

This protocol is set up to amplify the EBNA 2 region using primers shown in Table III.

**Table III.**

|   | Position    | Length       | GC (%) | Tm (C) |
|---|-------------|--------------|--------|--------|
| <b>Primers</b>                                    |             |              |        |        |
| GGCTGGTGTACCTGTTA (SEQ. ID. NO. 1)                | 90030:90049 | [[20]]<br>18 | 55     | 50     |
| CCTTAGGAGGAACAAGTCCC (SEQ. ID. NO. 2)             | 90249:90269 | 20           | 55     | 50     |
| <b>Product</b>                                    | 90030:90269 | 239          |        |        |
| <b>Hybridization Probes</b>                       |             |              |        |        |
| GGTGGAGGGCTGAGTGTCTCTGGGT-F red 640 (SEQ.ID.NO.3) | 90114:90139 | 25           | 64     | 71.8   |
| GAACGGGTCTCAGTGACATGGAAGA-p (SEQ. ID. NO. 4)      | 90142:90167 | 26           | 50     | 66.9   |

Other sequences that may be used include:

Primers:

(sense) AGGGATGCCTGGACACAAGA (SEQ. ID. NO. 5)

(antisense) ATTGCCACCACCAGCAGCACCA (SEQ. ID. NO. 6)

Probes

(1) CATCTGCTATGCGAATGCTTTG (SEQ. ID. NO. 7)

(2) GCTAATTATATTGTAAGACA (SEQ. ID. NO. 8)